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Amendments to Claims**Claims 1-5 (canceled)**

**Claim 6. (Currently Amended)** An isolated nucleic acid molecule as set forth in SEQ ID NO:18 wherein said nucleic acid molecule encodes *crtE*, *crtX*, *crtY*, *crtJ*, *crtB* and *crtZ* or comprising a an isolated nucleic acid molecule polynucleotide having at least 95% identity to SEQ ID NO:18, wherein said isolated nucleic acid molecule polynucleotides encodes the following enzymes : geranylgeranyl pyrophosphate synthase (*crtE*) phytoene synthase (*crtB*), phytoene desaturase (*crtJ*) lycopene cyclase (*crtY*),  $\beta$ -carotene hydroxylase (*crtZ*), and zeaxanthin glucosyl transferase, (*crtX*).

**Claims 7-13 (Canceled)**

**Claim 14 (Original).** A vector comprising the isolated nucleic acid molecule of Claim 6.

**Claim 15 (Canceled)**

**Claim 16 (Original).** A transformed host comprising the isolated nucleic acid molecule of claim 6.

**Claim 17 (Previously Presented).** The transformed host cell of Claim 16 wherein the host cell is selected from the group consisting of bacteria, yeast, filamentous fungi, algae, and green plants.

**Claim 18 (Original).** The transformed host cell of Claim 17 wherein the host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodosporidium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Torulopsis*, *Rhodotorula*, and *Phaffia*.

**Claim 19 (Canceled)**

**Claim 20 (Previously Presented).** A method for the production of carotenoid compounds comprising:

- (a) providing a transformed host cell comprising:
  - (i) suitable levels of farnesyl pyrophosphate; and
  - (ii) the isolated nucleic acid molecule of claim 6 under the control of suitable regulatory sequences;
- (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a fermentable carbon substrate whereby a carotenoid compound is produced.

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**Claim 21 (Previously Presented).** A method according to Claim 20 wherein the transformed host cell is selected from the group consisting of C1 metabolizing hosts, bacteria, yeast, filamentous fungi, algae, and green plants.

**Claim 22 (Previously Presented).** A method according to Claim 21 wherein the C1 metabolizing host is a methanotroph and the fermentable carbon substrate is selected from the group consisting of methane, methanol, formaldehyde, formic acid, methylated amines, methylated thiols, and carbon dioxide.

**Claim 23 (Original).** A method according to Claim 22 wherein the C1 metabolizing host:

- (a) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and
- (b) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate-dependent phosphofructokinase enzyme.

**Claim 24 (Original).** A method according to Claim 23 wherein the C1 metabolizing host cell is a high growth methanotrophic bacterial strain, known as *Methylomonas* 16a and having the ATCC designation PTA 2402.

**Claim 25 (Previously Presented).** A method according to Claim 20 wherein the transformed host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Yarrowia*, *Rhodosporidium*, *Lipomyces*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Flavobacterium*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Escherichia*, *Pantoea*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, *Methylophilus*, *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Torulopsis*, *Rhodotorula*, and *Phaffia*.

**Claim 26 (Previously Presented).** A method according to Claim 20, wherein the carotenoid compound produced is selected from the group consisting of,  $\beta$ -carotene, lycopene, pohytopene, zeaxanthin and zeaxanthin- $\beta$ -diglucoside.